

AMENDMENTS TO THE SPECIFICATION

At page 1 before the heading "Background of the Invention," please insert the following heading and paragraph:

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation-in-part of U.S. Application No. 10/604,943, filed August 28, 2003, and this application claims the benefit of U.S. Provisional Application No. 60/441,230, filed January 17, 2003; and U.S. Application No. 10/604,943 is a continuation-in-part of U.S. Application No. 10/604,942, filed August 27, 2003, and U.S. Application No. 10/604,943 claims the benefit of U.S. Provisional Application No. 60/441,241, filed January 17, 2003; and U.S. Application No. 10/604,942 is a continuation-in-part of U.S. Application No. 10/604,945, filed August 27, 2003, which is a continuation of U.S. Application No. 10/303,778, filed November 26, 2002.

Please replace paragraph [0051] with the following replacement paragraph:

FIG. 12A is an annotated sequence of EST72223 (SEQ ID NO: 415) comprising novel gene GAM24 (SEQ ID NO: 419) detected by the gene detection system of the present invention;

Please replace paragraph [0054] with the following replacement paragraph:

FIG. 13A is an annotated sequence of an EST7929020 (SEQ ID NO: 416) comprising novel genes GAM23 (SEQ ID NO: 420) and GAM25 (SEQ ID NO: 421) detected by the gene detection system of the present invention;

Please replace paragraph [0057] with the following replacement paragraph:

FIG. 14A is an annotated sequence of an EST1388749 (SEQ ID NO: 417) comprising novel gene GAM26 (SEQ ID NO: 422) detected by the gene detection system of the present invention;

Please replace paragraph [0066] with the following replacement paragraph:

VGAM PRECURSOR RNA folds onto itself, forming VGAM FOLDED PRECURSOR RNA. As FIG. 8 illustrates, VGAM FOLDED PRECURSOR RNA forms a "hairpin structure", folding onto itself. As is well known in the art, this "hairpin structure", is typical genes of the miRNA genes, and is due to the fact that nucleotide sequence of the first half of the RNA of a gene in this group is an accurate or partial inverted-reversed sequence of the nucleotide sequence of its second half. By "inversed-reversed" is meant a sequence which is reversed and

wherein each nucleotide is replaced by a complimentary nucleotide, as is well known in the art (e.g. ATGGC [SEQ ID NO: 407] is the inverted-reversed sequence of GCCAT [SEQ ID NO: 408]).

Please replace paragraph [0146] with the following replacement paragraph:

Reference is now made to FIG. 12A which is an annotated sequence of an EST comprising a novel gene detected by the gene detection system of the present invention. FIG. 12A shows the nucleotide sequence of a known human non-protein coding EST (Expressed Sequence Tag), identified as EST72223 (SEQ ID NO: 415). It is appreciated that the sequence of this EST comprises sequences of one known miRNA gene, identified as MIR98 (SEQ ID NO: 418), and of one novel GAM gene, referred to here as GAM24 (SEQ ID NO: 419), detected by the bioinformatic gene detection system of the present invention, described hereinabove with reference to FIG. 2.

Please replace paragraph [0151] with the following replacement paragraph:

Transcript preparations: Digoxigenin (DIG) labeled transcripts were prepared from EST72223 (TIGER), MIR98 and predicted precursor hairpins by using a DIG RNA labeling kit (Roche Molecular Biochemicals) according to the manufacturer's protocol. Briefly, PCR products with T7 promoter at the 5" end or T3 promoter at the 3" end were prepared from each DNA in order to use it as a template to prepare sense and antisense transcripts, respectively. MIR-98 was amplified using EST72223 as a template templet with T7miR98 forward primer: 5"-TAATACGACTCACTATAGGGTGAGGTAGTAAGTTGTATTGTT-3" (SEQ ID NO: 409) and T3miR98 reverse revse primer: 5"-AATTAACCCTCACAAAGGAAAGTAGTAAGTTGTAGTT-3" (SEQ ID NO: 410). EST72223 was amplified with T7-EST 72223 forward primer: 5"-TAATACGACTCACTATAGGCCCTTATTAGAGGATTCTGCT-3" (SEQ ID NO: 411) and T3-EST72223 reverse primer: 5"-AATTAACCCTCACTAAAGGTTTTTTTCCTGAGACAGAGT-3" (SEQ ID NO: 412). Bet-4 was amplified using EST72223 as a template templet with Bet-4 forward primer: 5"-GAGGCAGGA GAATTGCTTGA-3" (SEQ ID NO: 413) and T3-EST72223 reverse primer: 5"-AATTAACCCTCACTAAAGGCCTGAGACAGAGTCTTGCTC-3" (SEQ ID NO: 414). The PCR products were cleaned and used for DIG-labeled or unlabeled transcription reactions with the appropriate polymerase. For transfection experiments, CAP reaction was performed by using a mMassage mMachine kit (Ambion).

Please replace paragraph [0157] with the following replacement paragraph:

Reference is now made to FIG. 13A which is an annotated sequence of an EST comprising a novel gene detected by the gene detection system of the present invention. FIG. 13A shows the nucleotide sequence of a known human non-protein coding EST (Expressed Sequence Tag), identified as EST 7929020 (SEQ

ID NO: 416). It is appreciated that the sequence of this EST comprises sequences of two novel GAM genes, referred to here as GAM23 (**SEQ ID NO: 420**) and GAM25 (**SEQ ID NO: 421**), detected by the bioinformatic gene detection system of the present invention, described hereinabove with reference to FIG. 2.

Please replace paragraph [0160] with the following replacement paragraph:

Reference is now made to FIG. 14A which is an annotated sequence of an EST comprising a novel gene detected by the gene detection system of the present invention. FIG. 14A shows the nucleotide sequence of a known human non-protein coding EST (Expressed Sequence Tag), identified as EST 1388749 (**SEQ ID NO: 417**). It is appreciated that the sequence of this EST comprises sequence of a novel GAM gene, referred to here as GAM26 (**SEQ ID NO: 422**), detected by the bioinformatic gene detection system of the present invention, described hereinabove with reference to FIG. 2.

Please replace Table 2 with the following replacement Table 2:

GENE	G-SEQID	TARGET	UTR	SEQUENCE	T-SEQID	BINDING-SITE
GAM15	<u>423</u>	PRIM2A	3'	CAGGCAGATCTCAGACTC	50	C TCAGA GAGTC GAGATCT CCTG CTCAG CTCTAGA GGAC
GAM15	<u>424</u>	RAP1B	3'	CCAGGTCTGAAGAACTGTTGCC 142 CA		A C A CCG A TG GT AG TCTTCAGACCTGG AC CG TC AGAAGTCTGGACC
GAM15	<u>424</u>	RET	3'	CCAGGTCTAACACAGCTGACCCA 173		C TTG A A CG ATCTTC TG GTC AG AGACCTGG AC CAG TC TCTGGACC
GAM15	<u>424</u>	RET	3'	CCAGGTCTAACACAGCTGACCCA 174		C GACAAA A CG ATCTTC TG GTC AG AGACCTGG AC CAG TC TCTGGACC
GAM15	<u>424</u>	RET	3'	CCAGGTCTAACACAGCTGACCCA 179		C GACAAA A CG ATCTTC TG GTC AG AGACCTGG AC CAG TC TCTGGACC
GAM15	<u>424</u>	RET	3'	CCAGGTCTAACACAGCTGACCCA 37		C GACAAA A CG ATCTTC TG GTC AG AGACCTGG AC CAG TC TCTGGACC
GAM15	<u>425</u>	AMOTL1	3'	CTGATAAAAGATTCTAGACTCA 304		C GACAAA TGAGTC GAGATCT TCAG ACTCAG CTTTAGA AGTC
GAM15	<u>424</u>	DGKZ	3'	CCAGACCTAGGGCTGGACTCA	70	A AAT G A C AC TGAGTCC AG TCTT AG CTGG ACTCAGG TC GGGG TC GACC

GAM15	<u>426</u>	DKFZP586G1122	3'	CAGGTCTAGCCGGGCCA	265	- A - AGAT CA TG GTCCG CT AGACCTG AC CGGGC GA TCTGGAC C C — — A TGAGTCC ATCT TCAG CCTGG ACTCAGG TAGG AGTC GGACC TA C G ATCT AC — GAGTCC AG TCAG CT G CTCAGG TC GGTC GA C CC A — AGATCT AG TGAGTCCG TC ACCTGG ACTCAGGC AG TGGACC CCATCC — A CCG A TG GT AG TCTTCAGACCTGG AC CG TC AGAAAGTCTGGACC C TTG A A CCG A TG GT AG TCTTCAGACCTGG AC CG TC AGAAAGTCTGGACC C TTG A T C TTTTA AGA ATCACTATG AAAAT TCT TGGTGGTAC — A TTTTATAGAC TC CTATG AAAATGTCTG GG GATAC CG AC A TTTTATAGAC TCACATATG AGAATATTTG AGTGATAC AA CAC TTTTATAGACAT TATG AAGATATCTGTA GTAC AAA ATA A TTTT GAC TCACATATG AGAA CTG AGTGATAC GTC C C A TTTTATAGA ATC CTATG AAGATATCT TAG GATAC T CA — TTTTATAGACAT CTATG AAATATCTGTG GATAC TAA A TTTTATAG CA TCACATATG AAGATATC GT GGTGATAC C C
GAM15	<u>424</u>	FLJ22127	3'	CCAGGCCTGAATGGATGGACTC	192	A
GAM15	<u>423</u>	LOC126248	3'	CAGCCCTGGCTGGACTC	308	
GAM15	<u>424</u>	LOC146640	5'	CCAGGTGACCTACCCGGACTCA	323	
GAM15	<u>424</u>	LOC153416	3'	CCAGGTCTGAAGAACTGTTGCC	263	CA
GAM15	<u>424</u>	LOC220790	3'	CCAGGTCTGAAGAACTGTTGCC	378	CA
GAM16	<u>427</u>	PRKG2	3'	CATGGTGGTATCTTAAAA	103	
GAM16	<u>427</u>	AFAP	3'	CATAGCAGGGCGTCTGTAAAA	183	
GAM16	<u>427</u>	C3AR1	3'	CATAGTGAAAGTTTATAAGA	76	
GAM16	<u>427</u>	FLJ22029	3'	CATGAAAATGTCTATAGAA	203	
GAM16	<u>427</u>	SEMA5A	3'	CATAGTGACGTCTGAAGA	72	
GAM16	<u>427</u>	UNC5D	3'	CATAGGATTTCTATAGAA	234	
GAM16	<u>428</u>	LOC129446	3'	CATAGAATGTGTCTATAAA	315	
GAM16	<u>427</u>	LOC153396	3'	CATAGTGGCTGCCTATAGAA	338	

GAM16	<u>427</u>	LOC50999	3'	CATAATGGTGTCTTAAAA	145	T TTTTA AGACATCA TATG AAAT TCTGTGGT ATAC A
GAM17	<u>429</u>	KIAA0830	3'	AACATTATGCTTACTGCATC	290	A _ TA GAT CAG AGG CATAATGTT CTA GTC TTC GTATTACAA C A CAGA_
GAM17	<u>430</u>	PREI3	3'	AACATTATGTACTGTATATAC	275	ATGATA GGTACACATAATGTT TCATGTATTACAA
GAM17	<u>431</u>	SEC15L	3'	ACATATGCCTCTACTCATA	297	ATATG TAC CATA TATGA AGAGGTA ATGT ATACT TCTCCGT TACA
GAM17	<u>432</u>	LOC152317	3'	AACATCAATGGACTCTGTATCA	352	CA_ A TGATACAGAG CAT ATGTT ACTATGTCTC GTA TACAA AG_ AC
GAM18	<u>433</u>	DSCR1	3'	CATTTGAAATACTTAA	81	TT TTAACGTGTTCAA GTG AATTCAAAAGTT TAC
GAM18	<u>434</u>	ELMO2	3'	CCAGGAGAACACTTA	235	T AA TAAGTGTTC TT TGG ATTCACAAAG AG ACC
GAM18	<u>434</u>	ELMO2	3'	CCAGGAGAACACTTA	186	G AA G TAAGTGTTC TT TGG ATTCACAAAG AG ACC
GAM18	<u>435</u>	FGF5	3'	CCACAGGGAGCAAACACTTAG	227	G CAA TTAACGTGTTT TTGTGG GATTCAACAAA GACACC
GAM18	<u>435</u>	FGF5	3'	CCACAGGGAGCAAACACTTAG	83	CGAGG CAA TTAACGTGTTT TTGTGG GATTCAACAAA GACACC
GAM18	<u>435</u>	NEFH	3'	CCACACGTAAACACTTGA	180	CGAGG CAAT TTAACGTGTTT TGTGG AGTTCAACAAA ACACC
GAM18	<u>435</u>	NFIB	3'	CCACAAAAGAACACTTAA	93	TGC AA TTAACGTGTTT TTGTGG AATTCAACAAAG AACACC
GAM18	<u>435</u>	PRKY	3'	CCATAAAATGAAACACTTGA	62	AA A TTAACGTGTTCA TTGTGG AGTTCAACAAAGT AATACC A
GAM18	<u>434</u>	RNF18	5'	CCACAATTGGTTCTTA	172	TGT TAAG TTCAATTGTGG ATTC GGGTTAACACC
GAM18	<u>435</u>	SLC1A3	3'	CCACAATTGAAATTTTAA	77	TT T

						TTAAG GTTTCAATTGTGG AATTT TAAAGTTAACACC T
GAM18	<u>435</u>	VMD2	3'	CCATTGGAAACATTTAA	78	AATT TTAAGTGTTC GTGG AATTACAAAG TACC
GAM18	<u>435</u>	XRCC3	5'	CCAGGGAGACACTTAA	91	GT AAT G TTAAGTGTTC T TGG AATTACAGAG G ACC G
GAM18	<u>435</u>	ARHGAPS	3'	CTATATGAAACATTTAA	321	AT TTAAGTGTTC TGTGG AATTACAAAGT ATATC
GAM18	<u>435</u>	EFA6R	3'	CCATTGTGAAACACTTAA	140	ATT TTAAGTGTTC CA GTGG AATTACAAAGT TACC
GAM18	<u>434</u>	KIAA0903	3'	CCACATGTAACACTTA	294	GT T AT TAAGTGT CA TGTGG ATTCACAA GT ACACC T —
GAM18	<u>436</u>	KIAA1244	3'	CCACAAATTGTCGAACAT	295	GTGTTT CAATTGTGG TACAAG GTTAACACCC TCT
GAM18	<u>435</u>	Rpol-2	3'	CTGTGGTAAGAACACTTAA	214	CA TG TTAAGTGT TT TGG AATTACAAAG TG GTC AA GT AA
GAM18	<u>435</u>	LOC115574	3'	CCACAACTGGAAACACTTGA	303	TTAAGTGTTC TTGTGG AGTTCACAAAG AACACC GTC
GAM18	<u>434</u>	LOC144144	5'	CCACAAATTGGGTTCTTA	260	TGT TAAG TTCAATTGTGG ATTC GGGTTAACACCC TT —
GAM18	<u>435</u>	LOC148254	3'	CCATCAAAAGAACACTTAA	329	AA TTAAGTGTTC TTG TGG AATTACAAAG AAC ACC AA T ATT
GAM18	<u>435</u>	LOC157624	5'	CCACTGAAACATTTAA	359	TTAAGTGTTC GTGG AATTACAAAG CACC
GAM18	<u>434</u>	LOC220486	5'	CCACAAATTGGGTTCTTA	374	TGT TAAG TTCAATTGTGG ATTC GGGTTAACACCC TT —
GAM19	<u>437</u>	AGL	3'	ATGCTTCATTTTTCACTG	31	AA A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA A C AA A CAG GAAAAAAT AAAGCAT
GAM19	<u>437</u>	AGL	3'	ATGCTTCATTTTTCACTG	43	

GAM19	<u>437</u>	AGL	3'	ATGCTTTCA TTT TTCACTG	44	 GTC CTTTTTTA TTTCGTA A_ C AA A CAG GAAAAAAAT AAAGCAT
GAM19	<u>437</u>	AGL	3'	ATGCTTTCA TTT TTCACTG	45	 GTC CTTTTTTA TTTCGTA A_ C AA A CAG GAAAAAAAT AAAGCAT
GAM19	<u>437</u>	AGL	3'	ATGCTTTCA TTT TTCACTG	46	 GTC CTTTTTTA TTTCGTA A_ C AA A CAG GAAAAAAAT AAAGCAT
GAM19	<u>437</u>	AGL	3'	ATGCTTTCA TTT TTCACTG	47	 GTC CTTTTTTA TTTCGTA A_ C AA A CAG GAAAAAAAT AAAGCAT
GAM19	<u>438</u>	ALB	5'	GCTTTCTCTTCTGTCA	40	A_ C AAAAAT TGACAGAAGA AAAAGC ACTGTCTTCT TTTCG
GAM19	<u>439</u>	CKN1	3'	TTTATTCTTTCTTCTTCA	32	C_ A TGA AGAAGAAA ATAAAAA ACT TCTTCTTT TTATTTT C
GAM19	<u>440</u>	HHIP	3'	TTTATT TTT TATCCTGTCA	189	- AAG TGACAG AAAAAATAAA ACTGTC TTTTTATTT CTA GAAAAA A
GAM19	<u>438</u>	IFNA1	3'	GCTTTCATGAATTCTGTCA	194	TGACAGAA AT AAAGC ACTGTCTT TA TTTCG AAG C
GAM19	<u>439</u>	KCNJ6	5'	TTTTTTTTTTCTTCTGCCA	60	A T TG CAGAAGAAAAA AAAA AC GTCTTCTTTTT TTTT C C T C GA GA AGAA AAAATAAAAGC CT TTTT TTTTTATTTCG A A_ TAA
GAM19	<u>441</u>	OTP	3'	GCTTTATTTTATTTATC	212	TGACAGAAGAAAAA AAGCAT ATTGTCTTCTTTTT TTTCGTA C_
GAM19	<u>442</u>	RHEB2	3'	ATGCTTCTTTTCTTGTAA	94	AGAAAA TGACAGA AATAAAAGCAT ATTGTCTT TTATTTTCGTA CCC_ ATAAAAA
GAM19	<u>442</u>	ANKRD6	3'	ATGCTTTATTCCCTTGTAA	137	TGA AGAAGAAAAA GCA ACT TCTTCTTTTT CGT - G TA GGA TGACA AAGAAAAA AAAGCAT
GAM19	<u>443</u>	EVI5	3'	TGCAGGTTTTCTTCTTCA	95	 TGACAGAAGAAAAA AAGCAT
GAM19	<u>442</u>	FLJ00026	3'	ATGCTTGC TTT TTCTTATG	270	 TCA

GAM19	<u>442</u>	GP5	3'	ATGCTCATATCATTTCCTCT 84	ACTGT TTCTTTTT TTTCGTA A TCG C AA TGA AGAAGAAAAA ATA AGCAT ACT TCTTCTTTTT TAT TCGTA C AC AC C AAA GA AGAAGAAAAAAT AGCAT TT TCTTTTTTTTG TCGTA C A AAAATAAA TGACAGAA GAA AGCA ACTGTCTT CTT TCGT T GTG AAAATAA ACAGAAGA AAAGCAT TGTCTTCTT TG TTTCGTA CCAATA AAAAA TGACAGAAGAAAAAT GC ACTGTCTTCTTTTG TG CCGG TAAAAA ACAGAAGAAAAA GCAT TGTCTTCTTTTG CGTA TTAC AAATAA GACAGAAGAAA AAAGC CTGTCTTCTTT TG TTTCG CTCA AA TGACAG GAAAAAATAA ACTGTT CTTTTTATT C ATAAAAA TGACAGAAGAAAA GCAT ATTGTCTTCTTT TGTA CGAG A TGACAGAAGAAA ATAA ATTGTCTTCTTT TATT C A TGACAGAAGAAA ATAA ATTGTCTTCTTT TATT C AAA TGACAGAAGA AATAA ACTGTCTTCTT TTATT ATC AAAAAATAA TGACAGAAG AAGCAT ACTGTCTTCTT TTTGTA CTCTCA CA A AA TGA GA GA AAATAAAAGCA ACT CT CT TTTATTTTCGT
GAM19	<u>444</u>	KHDRBS3	3'	ATGCTAGTTTTTTCTCTT 107	
GAM19	<u>443</u>	KIAA0254	3'	TGCTGTGTTCTTCTGTCA 132	
GAM19	<u>445</u>	KIAA1165	3'	ATGCTTTATAACCTCTCTGT 281	
GAM19	<u>438</u>	KIAA1240	3'	GTGGCCATTTTCTCTGTCA 277	
GAM19	<u>445</u>	NYD-SP15	3'	ATGCCATTTTCTCTGT 209	
GAM19	<u>441</u>	PELI1	5'	GCTTTACTCTTCTGTCA 175	
GAM19	<u>446</u>	PRO0159	5'	TTATTTTTCTTGTCA 125	
GAM19	<u>442</u>	RACGAP1	3'	ATGTGAGCTTTCTCTGTAA 121	
GAM19	<u>446</u>	SDFR1	3'	TTATCTTTCTCTGTAA 118	
GAM19	<u>446</u>	SDFR1	3'	TTATCTTTCTCTGTAA 151	
GAM19	<u>446</u>	SS18L1	3'	TTATTCTATCTCTGTCA 272	
GAM19	<u>442</u>	SV2B	3'	ATGTTTACTCTCCTCTGTCA 136	
GAM19	<u>443</u>	LOC130589	3'	TGCTTTATTCCTCCTCCTTC 244	

GAM19	<u>447</u>	LOC200107 3'	ATGCTTTTACTTTTCTTT	364	TC C CC A AGAAGAAAAA TAAAAGCAT TTTCTTTT ATTTCGTA C	
GAM19	<u>448</u>	LOC203340 3'	TGCTTTTATTTCCTTC	368	AA GAAG AAAATAAAAGCA CTTC TTTTATTTTCGT C_	
GAM19	<u>443</u>	LOC221271 3'	TGCCTTTTTCTGTCA	380	ATAAAAA TGACAGAAGAAAAA GCA ACTGTCTTTTTTT CGT C	
GAM19	<u>442</u>	LOC254778 3'	ATGCTTTCTCTATCA	400	C AAATAAA TGA AGAAGAAA AGCAT ACT TCTTCTTT TCGTA A	
GAM19	<u>449</u>	LOC51312 5'	GCTTTTATTTCCTCCTCT	164	A A AGA GA AAAATAAAAGC TCT CT TTTTATTTCG C C	
GAM19	<u>450</u>	LOC91286 5'	TTTTTATTCTTTCTGTCA	273	A TGACAGAAGAA AAATAAAAG ACTGTCTTTT TTATTTTT C	
GAM19	<u>451</u>	LOC92223 3'	ATGCTTTATTGTACCTTC	286	AAAAA GAAG AATAAAAGCAT CTTC TTATTTTCGT CATG	
GAM19	<u>452</u>	LOC92482 5'	TGCATCTTCTCTGT	288	A AAAA ACAGAAGAAA AT GCA TGTCTTCTTT TA CGT C	
GAM20	<u>453</u>	ATRN	3'	CTATCTGATGCACAGAA	248	G AAG TT TGTGCATCA GATAG AA ACACGTAGT CTATC G
GAM20	<u>453</u>	ATRN	3'	CTATCTGATGCACAGAA	248	G AAG TT TGTGCATCA GATAG AA ACACGTAGT CTATC G
GAM20	<u>454</u>	DKFZP56400463 3'	CTTTTCTTAATGCATACAATA	127	CAA T TATTGTGTGCAT AGGA AGAG ATAACATACGTA TTCT TTTC A T	
GAM20	<u>454</u>	DKFZP56400463 3'	CTTTTCTTAATGCATACAATA	127	CAA T TATTGTGTGCAT AGGA AGAG ATAACATACGTA TTCT TTTC A T	
GAM20	<u>454</u>	FLJ13102	3'	CTCTACCCCTCTCCCACCACACA	202	CATCAA A TATTGTGTG AGG TAGAG ATGACACAC TCC ATCTC CACCCTC C
GAM20	<u>454</u>	FLJ13102	3'	CTCTACCCCTCTCCCACCACACA	202	CATCAA A TATTGTGTG AGG TAGAG ATGACACAC TCC ATCTC CACCCTC C

GAM20	<u>453</u>	HSPC014	3'	CTGTAATTTGATGTACACAA	144	GG TTGTGTGCATCAAA ATAG AACACATGTAGTTT TGTC
GAM20	<u>454</u>	HSPC014	3'	CTGTAATTTGATGTACACAA	144	AA GG TTGTGTGCATCAAA ATAG AACACATGTAGTTT TGTC
GAM20	<u>455</u>	KIAA0040	3'	TCTATCCCCTGTCACATA	129	AA TCAAA TGTGTG CA GGATAGA ATACAC GT CCTATCT
GAM20	<u>455</u>	KIAA0040	3'	TCTATCCCCTGTCACATA	129	T TCC TCAAA TGTGTG CA GGATAGA ATACAC GT CCTATCT
GAM20	<u>456</u>	KIAA0470	3'	CCACTTGATGCACAAATA	134	T TCC G A TATT TGTGCATCAA GG ATAA ACACGTAGTT CC
GAM20	<u>456</u>	KIAA0470	3'	CCACTTGATGCACAAATA	134	CA G A TATT TGTGCATCAA GG ATAA ACACGTAGTT CC
GAM20	<u>457</u>	KIAA1908	5'	CTCTCGGGCGATGCACACAA	302	CA AAAGGAT TTGTGTGCATC AGAG AACACACGTAG TCTC
GAM20	<u>457</u>	KIAA1908	5'	CTCTCGGGCGATGCACACAA	302	CGGGC AAAGGAT TTGTGTGCATC AGAG AACACACGTAG TCTC
GAM20	<u>454</u>	MGC22014	3'	CTCTATCCTTGTATATCACAAAT	269	CGGGC TGCATCA TATTGTG AAGGATAGAG ATAACAC TTCCCTATCTC
GAM20	<u>454</u>	MGC22014	3'	CTCTATCCTTGTATATCACAAAT	269	TATATG TGCATCA TATTGTG AAGGATAGAG ATAACAC TTCCCTATCTC
GAM20	<u>453</u>	TNRC9	3'	CTGTATTTGATGCAACAA	293	TATATG G G TTGT TGCATCAAAG ATAG AACAC ACGTAGTTT TGTC
GAM20	<u>453</u>	TNRC9	3'	CTGTATTTGATGCAACAA	293	A G G TTGT TGCATCAAAG ATAG AACAC ACGTAGTTT TGTC
GAM20	<u>454</u>	LOC116123	3'	CTTTGGTTTGATGCATACAATA	243	A GGA TATTGTGTGCATCAA TAGAG ATAACACATACGTAGTTT GTTTC
GAM20	<u>454</u>	LOC116123	3'	CTTTGGTTTGATGCATACAATA	243	G GGA TATTGTGTGCATCAA TAGAG ATAACACATACGTAGTTT GTTTC
GAM20	<u>458</u>	LOC149721	3'	CTATCATGTGGATGCACACA	334	G AAAG_

			TGTGTGCATC	GATAG
			ACACACGTAG	CTATC
			GTGTA	
GAM20	<u>458</u>	LOC149721 3'	CTATCATGTGGATGCACACA	334
			AAAG	
			TGTGTGCATC	GATAG
			ACACACGTAG	CTATC
			GTGTA	
GAM20	<u>454</u>	LOC153338 5'	CTCTATCCCTCTGTGGCCAATA	354
			T G CAAA	
			TATTG GT CAT	GGATAGAG
			ATAAC CG GTG	CCTATCTC
			T TCTC	
GAM20	<u>454</u>	LOC153338 5'	CTCTATCCCTCTGTGGCCAATA	354
			T G CAAA	
			TATTG GT CAT	GGATAGAG
			ATAAC CG GTG	CCTATCTC
			T TCTC	
GAM20	<u>456</u>	LOC220766 3'	CCACTTGATGCACAAATA	375
			G A	
			TATT TGTGCATCAA GG	
			ATAA ACACGTAGTT CC	
			CA	
GAM20	<u>456</u>	LOC220766 3'	CCACTTGATGCACAAATA	375
			G A	
			TATT TGTGCATCAA GG	
			ATAA ACACGTAGTT CC	
			CA	
GAM20	<u>453</u>	LOC253351 5'	CTGGCACCTGATGCACACAA	402
			AAGGA	
			TTGTGTGCATCA TAG	
			AACACACGTAGT GTC	
			CCACG	
GAM20	<u>453</u>	LOC253351 5'	CTGGCACCTGATGCACACAA	402
			AAGGA	
			TTGTGTGCATCA TAG	
			AACACACGTAGT GTC	
			CCACG	
GAM20	<u>454</u>	LOC257484 3'	CTCTATCCTTGTATATCACAAAT	366
		A	TGCATCA	
			TATTGTG AAGGATAGAG	
			ATAAACAC TTCCTATCTC	
			TATATG_	
GAM20	<u>454</u>	LOC257484 3'	CTCTATCCTTGTATATCACAAAT	366
		A	TGCATCA	
			TATTGTG AAGGATAGAG	
			ATAAACAC TTCCTATCTC	
			TATATG_	
GAM21	<u>459</u>	KIAA1843 3'	ATAGAAAGTAGCCAAAAAA	267
			CTG	
			TTTTTG TACTTTCTAT	
			AAAAAC ATGAAAGATA	
			CG_	
GAM21	<u>460</u>	SDFR1 3'	AAAGTACAGCAAAACCTA	117
			T	
			TAG TTTTGCTGTACTTT	
			ATC AAAACGACATGAAA	
			C	
GAM21	<u>460</u>	SDFR1 3'	AAAGTACAGCAAAACCTA	150
			T	
			TAG TTTTGCTGTACTTT	
			ATC AAAACGACATGAAA	
			C	
GAM21	<u>461</u>	LOC132617 3'	CTACAGACCATAGCAAAAC	314
			ACTT A	
			GTGTTTGCTGT TCT TAG	
			CAAAACGATA AGA ATC	
			CC_ C	
GAM21	<u>461</u>	LOC145622 3'	CTATAGAACATGCACAAAC	322
			TGTACT	
			GTGTTTGCTC TTCTATAG	

GAM21	<u>462</u>	LOC222681	3'	CTACAGAACATGGAGCAAAAC	386	TA CAAAAACG TAAC G CT A TAGTTTTGCT TA TTCT TAG ATCAAAACGA GT AAGA ATC G AC C G CT A TAGTTTTGCT TA TTCT TAG ATCAAAACGA GT AAGA ATC G AC C G CT A TAGTTTTGCT TA TTCT TAG ATCAAAACGA GT AAGA ATC G AC C G CA AGATGGTG AGTGGT TCTACCTAC TCACCA A T CAA AAGATGGG GG GTGGT TTCTACTT CC CACCA TC CA_ T AGATGGTG AG GGT TCTACCCACC TC CCA CCG — GATGG GTGGCAAGTGGT TTGTC CACCGTTACCA G G C AGATGG TGG AAGTGGT TTTACC ACT TTCACCA G T GGCA TAAGATGGT AGTGGT GTTCTACTCA TCACCA GC GGTGG TAAGATG CAAGTGGT ATTTTAC GTTCACCA AAA GTGGC TAAGATGG AAGTGGT ATTCTATT TTCACCA AAAA T A TAAGATGGG GGC AGTGGT GTTCTACCC CCG TCACCA GGGC T C AGATGGG GG AAGTGGT TCTACTT TC TTCACCA T T T AGA GGG GGCAAGTGGT
GAM21	<u>462</u>	LOC257507	3'	CTACAGAACATGGAGCAAAAC	405	TA ATCAAAACGA GT AAGA ATC G AC C G CT A TAGTTTTGCT TA TTCT TAG ATCAAAACGA GT AAGA ATC G AC C G CT A TAGTTTTGCT TA TTCT TAG ATCAAAACGA GT AAGA ATC G AC C G CA AGATGGTG AGTGGT TCTACCTAC TCACCA A T CAA AAGATGGG GG GTGGT TTCTACTT CC CACCA TC CA_ T AGATGGTG AG GGT TCTACCCACC TC CCA CCG — GATGG GTGGCAAGTGGT TTGTC CACCGTTACCA G G C AGATGG TGG AAGTGGT TTTACC ACT TTCACCA G T GGCA TAAGATGGT AGTGGT GTTCTACTCA TCACCA GC GGTGG TAAGATG CAAGTGGT ATTTTAC GTTCACCA AAA GTGGC TAAGATGG AAGTGGT ATTCTATT TTCACCA AAAA T A TAAGATGGG GGC AGTGGT GTTCTACCC CCG TCACCA GGGC T C AGATGGG GG AAGTGGT TCTACTT TC TTCACCA T T T AGA GGG GGCAAGTGGT
GAM21	<u>462</u>	LOC257625	3'	CTACAGAACATGGAGCAAAAC	406	TA ATCAAAACGA GT AAGA ATC G AC C G CT A TAGTTTTGCT TA TTCT TAG ATCAAAACGA GT AAGA ATC G AC C G CA AGATGGTG AGTGGT TCTACCTAC TCACCA A T CAA AAGATGGG GG GTGGT TTCTACTT CC CACCA TC CA_ T AGATGGTG AG GGT TCTACCCACC TC CCA CCG — GATGG GTGGCAAGTGGT TTGTC CACCGTTACCA G G C AGATGG TGG AAGTGGT TTTACC ACT TTCACCA G T GGCA TAAGATGGT AGTGGT GTTCTACTCA TCACCA GC GGTGG TAAGATG CAAGTGGT ATTTTAC GTTCACCA AAA GTGGC TAAGATGG AAGTGGT ATTCTATT TTCACCA AAAA T A TAAGATGGG GGC AGTGGT GTTCTACCC CCG TCACCA GGGC T C AGATGGG GG AAGTGGT TCTACTT TC TTCACCA T T T AGA GGG GGCAAGTGGT
GAM22	<u>463</u>	BTEB1	3'	ACCACTACATCCATCT	53	
GAM22	<u>464</u>	CEP2	3'	ACCACTCCTTCATCTT	112	
GAM22	<u>463</u>	ECM1	3'	ACCCCTGCCCAACCCATCT	82	
GAM22	<u>465</u>	ENG	3'	ACCACTTGCCACGCTGTT	34	
GAM22	<u>463</u>	ESRRG	3'	ACCACTTTTCAGCCATT	276	
GAM22	<u>466</u>	HDAC4	3'	ACCACTCGACTCATCTT	98	
GAM22	<u>466</u>	IL6	3'	ACCACTTGAAACATT	41	
GAM22	<u>466</u>	LRAT	3'	ACCACTTAAAATTATCTT	259	
GAM22	<u>466</u>	MYLK2	3'	ACCACTCGGGCCCCATCTT	226	
GAM22	<u>463</u>	PRKACB	3'	ACCACTTCTTTCATCT	61	
GAM22	<u>463</u>	PRLR	3'	ACCACTTGCTCTTTCT	51	

GAM22	<u>464</u>	SLC6A6	3'	ACCACTTGAATTGATCTT	65	TCT TCT CCGTTCACCA T G - GG AAGAT GGT CAAGTGGT TTCTA TTA GTTCACCA G A_- GGG
GAM22	<u>466</u>	WASF3	3'	ACCACTTGGTCAGAATTTA	109	TAAGAT TGGC AAGTGGT ATTTTA ACTG TTTCACCA AG - G TG - G TAAGA GGTG CAAGTGGT ATTCT TCAC GTTCACCA
GAM22	<u>466</u>	XK	3'	ACCACTTGCACTATTCTTA	181	TA A T - A AG TGGG GGCA GTGGT TC ACCC CCGT CACCA C - C CA - T AGATGGGTGG AG GGT TCTACCCACC TC CCA
GAM22	<u>463</u>	ZYX	3'	ACCACCTGCCACACCT	69	AGG CAA - TAAGATGGGTGG GTG ATTTTACCCACC CGC
GAM22	<u>463</u>	ARHF	3'	ACCCCTGGACCACCCATCT	167	A CAA TAAGATGGGTGG GTG ATTTTACCCACC CGC
GAM22	<u>467</u>	DDR1	5'	CGCACCAACCCATTITA	57	A CAA TAAGATGGGTGG GTG ATTTTACCCACC CGC
GAM22	<u>467</u>	DDR1	5'	CGCACCAACCCATTITA	122	A CAA TAAGATGGGTGG GTG ATTTTACCCACC CGC
GAM22	<u>467</u>	DDR1	5'	CGCACCAACCCATTITA	123	A CAA TAAGATGGGTGG GTG ATTTTACCCACC CGC
GAM22	<u>466</u>	DKFZP547E1010	5'	ACCACCTCCCTATCTTA	141	A TG CAA TAAGATGGG G GTGGT ATTCTATCC C CACCA
GAM22	<u>466</u>	DKFZP547E1010	5'	ACCACCTCCCTATCTTA	280	CT TG CAA TAAGATGGG G GTGGT ATTCTATCC C CACCA
GAM22	<u>463</u>	FLJ11715	3'	ACCGCGCCCAGCCCCATCT	197	CT — AA AGATGGGT GGC GTGGT TCTACCCG CCG CGCCA
GAM22	<u>463</u>	FLJ12587	3'	ACCAGGGCCGCATCCCATCT	190	AC — AAG AGATGG — GTGGC TGGT TCTACC CGCCG ACCA
GAM22	<u>465</u>	FLJ12650	3'	ACCACTTGCCAATGCCTCTC	196	TA GG_— GA GGGT — GGCAAGTGGT CT TCCG CCGTTCACCA C TAA
GAM22	<u>468</u>	FLJ13265	3'	ACCACTTGCCCTGCCTCA	201	TG GGT — GGCAAGTGGT AC CCG CCGTTCACCA

GAM22	<u>463</u>	FLJ20546	3'	ACCTCTGCCACCCATCT	155	T TC A T AGATGGGTGGCA G GGT TCTACCCACCGT C CCA T
GAM22	<u>466</u>	FLJ32865	3'	ACCACACGCCAGCTTA	251	A GCAA TAAG TGGGTG GTGGT ATTC ACCCGC CACCA G AC G TG AGATG G GCAAGTGGT TCTAC T TGTTCACCA A GT
GAM22	<u>463</u>	GPR88	3'	ACCACTTGTGTACATCT	185	AGT AGATGGGTGG CA GGT TTTACCCACC GT CCA
GAM22	<u>463</u>	HSPC216	3'	ACCTGACCACCCATT	149	A T CAA TAAGATGGG GG GTGGT ATTTTACCC CT CACCA
GAM22	<u>466</u>	JIK	3'	ACCACATTCCCCATT	148	TA A G AA TAAG TGGT GC GTGGT ATTC GCG CG CACCA C AA ACC G CAAG TAAGATGG TGG TGTT ATTCTACC ACC ACCA — AGAGG
GAM22	<u>466</u>	KIAA0153	3'	ACCACCCAGCAAGGCCGCCTTA	139	TGGGT ACCTA TTGTTCACCA AAG
GAM22	<u>466</u>	KIAA0215	3'	ACCAGGAGACCACCATCTTA	130	GGCAA TAAGATGGGT GTGGT ATTCTACTCA CACCA GA
GAM22	<u>468</u>	KIAA0461	3'	ACCACTTGTGAAATCCA	291	AGTGGT ACCTA TTGTTCACCA AAG
GAM22	<u>466</u>	MEGF10	3'	ACCACAGACTCATCTTA	216	GGCAA TAAGATGGGT GTGGT ATTCTACTCA CACCA GA
GAM22	<u>468</u>	MGC2452	5'	ACCACTAATTGCCACTCA	218	AGTGGT ACTCACCGT TCACCA TAA
GAM22	<u>466</u>	MGC4796	3'	ACCTTCACCTCATCTTA	266	CAAGT TAAGATG GGTGG GGT ATTCTAC CCACT CCA T T G
GAM22	<u>463</u>	MRPL10	3'	ACCACATTGTACCCATT	256	AGATGGGTG CAA GTGGT TTTACCCAT GTT CACCA A
GAM22	<u>466</u>	MRPL42	5'	ACCACTTGATAAGCATCTG	299	GG G TAAGATG TG CAAGTGGT GTTCTAC AT GTTCACCA GA A
GAM22	<u>464</u>	POLYDOM	3'	ACCACTGCTATCCATCTT	195	A AAGATGGGTGGCA GTGGT TTCTACCTATCGT CACCA

GAM22	<u>463</u>	PRO0246	5'	ACCACTTGCTATGGTCT	126	GG AGAT GTGGCAAGTGGT TCTG TATCGTTACCA
GAM22	<u>466</u>	SMCR7	3'	ATGACTTGCCACCCACCT	247	G_ A G AG TGGGTGGCAAGT GT TC ACCCACCGTTCA TA C G
GAM22	<u>466</u>	TPD52	3'	ACCACTTATATCAACTTA	88	ATG GC TAAG GGTG AAGTGGT ATTC CTAT TTCACCA AA_ A_ CA
GAM22	<u>464</u>	ZNF384	3'	ACCAACTCATCACGGCCATCTT	239	AAGATGG GTGG AGTGGT TTCTTACCA CACT TCACCA GG AC CA T
GAM22	<u>466</u>	LOC124216	3'	ACCTCTCCTCACCCATCTTA	307	TAAGATGGGTGG AG GGT ATTCTACCCACT TC CCA CC T AA
GAM22	<u>463</u>	LOC144509	5'	ACCAACCAGCTGCACCCATCT	320	AGATGGGTG GC GTGGT TCTACCCAC CG CACCA GT AC
GAM22	<u>463</u>	LOC146822	3'	ACCAACCTGCCCTACCATTT	324	GT A AGATGG GGCA GTGGT TTTACCC CCGT CACCA ATC C G C
GAM22	<u>463</u>	LOC148371	5'	ACCACTTCTGGCCATCT	330	AGATGG TGG AAGTGGT TCTACC GTC TTCACCA G
GAM22	<u>464</u>	LOC149373	3'	ACCTGCCGGCCACCCATTCA	333	A AA A GATGGGTGGC GT GGT A TTACCCACCG CG CCA C GC T CAAGT
GAM22	<u>466</u>	LOC151146	5'	ACCCCCCAGCCCATCTTA	336	TAAGATGGG TGG GGT ATTCTACCC ACC CCA G CC G CAA
GAM22	<u>466</u>	LOC157562	5'	ACCAACCCAGTCATTITA	357	TAAGATGG TGG GTGGT ATTTTACT ACC CACCA G
GAM22	<u>466</u>	LOC160897	3'	ACCACTTATAATGCCTCATCTT	341	GC TAAGATG GGTG AAGTGGT ATTCTAC CCGT TTCACCA T ATA G A
GAM22	<u>463</u>	LOC161589	5'	ACCACTGCTGGCCATCT	343	AGATGG TGGCA GTGGT TCTACC GTCGT CACCA G
GAM22	<u>468</u>	LOC163682	5'	ACCACTTGCCGAGCTCCTA	361	TGGG TGGCAAGTGGT ATCC GCCGTTACCA TCGA G AAG
GAM22	<u>466</u>	LOC199692	3'	ACCAAGTAACCTATCTTA	257	

GAM22	<u>463</u>	LOC202108	5'	ACCACTACTGGCCATCT	367	TAAGATGGGT ATTCTATCCA	GC TG	TGGT ACCA
GAM22	<u>464</u>	LOC221468	3'	ACCACCCAGTTCTTCATCTT	258	G AGATGG TCTACC	CA TGG GTC	A AGTGGT TCACCA
GAM22	<u>463</u>	LOC221838	5'	ACCACTACTGGCCATCT	385	G AGATGG TCTACC	CA TGG GTC	A AGTGGT TCACCA
GAM22	<u>463</u>	LOC221839	5'	ACCACTACTGGCCATCT	384	G AGATGG TCTACC	A G CA TGG GTC	A AGTGGT TCACCA
GAM22	<u>465</u>	LOC90313	5'	ACCACCCCTGTGCCCATC	268	G GATGGGTG CTACCCGT	A CA G A	C GTGGT CACCA
GAM22	<u>466</u>	LOC92399	3'	ACCACCTGCTCCTCATCTTA	242	CCC TG TAAGATGGG ATTCTACTC	A GCA CGT	A GTGGT CACCA
GAM23	<u>469</u>	ADAM8	3'	AGAGAAGCCATGCGTTCC	52	A C GAC T C TTG C C	T CAA CAT GTA C	T CT C CGT C
GAM23	<u>469</u>	BN51T	3'	AGAGAGCAAGGATTGAGTCTG	363	CAGACTCA GTCTGAGT	AA TC AG	T CTCT CGA GAGA
GAM23	<u>469</u>	CD3Z	3'	AGACTGACCTTGATGAGCTG	48	A CAG T GTC	C CTCATCAAG TT GAGTAGTTC	C C TCT AG AGA
GAM23	<u>470</u>	DAAM2	3'	AGGTGCTTGATGAATCTG	381	-C CAGA T GTCT	T TCATCAAGC TCT AGTAGTTCG	GAA TCT GGA
GAM23	<u>471</u>	DLG4	3'	AGGGAGGGATGGGTCT	54	A AGACTCATC T TCTGGGTAG	AAG CTTCTCT GGAGGGAA	T C TC A
GAM23	<u>472</u>	DMD	5'	AGAAAAGCTTGAGCAAGTC	73	CA GACT CTGA	— TCAAGCTT AGTCGAA	C TCT AGA
GAM23	<u>472</u>	DMD	5'	AGAAAAGCTTGAGCAAGTC	74	ACG CA CTGA	A CA AGTCGAA	A C AGA
GAM23	<u>472</u>	DMD	5'	AGAAAAGCTTGAGCAAGTC	75	ACG CA GACT	A CA TCAAGCTT	A C TCT

							CTGA	AGTCGAA	AGA
GAM23	<u>473</u>	E2F1	3'	AGGCCTCTTGAGCCTG	348		ACG	A	
							A		
							CAG	CTCATCAA	GCTT
							GTC	GAGTGGTT	CGGA
GAM23	<u>471</u>	EBP	3'	AGAGAACCCAGGAGGTCT	108		C	TCTC	
							CA	AA	
							AGACT	TC	GCTTCTCT
							TCTGG	AG	CGAAGAGA
GAM23	<u>472</u>	FANCG	5'	AGAGAACCCAGGGAGCTC	85		GAC		
							—	A	AA
							GA	CTC	TCT
							CT	GAG	GG
GAM23	<u>470</u>	FE65L2	5'	AGGCCTGATGAGTTCA	99		CGAAGAGA		
							C	—	GA
							A	A	T
							C	GACTCATCA	GC
									TCT
							A	TTGAGTAGT	CG
GAM23	<u>470</u>	FE65L2	5'	AGGCCTGATGAGTTCA	236		GGA		
							C	C	C
							A	A	T
							C	GACTCATCA	GC
									TCT
							A	TTGAGTAGT	CG
GAM23	<u>470</u>	FE65L2	5'	AGGCCTGATGAGTTCA	237		GGA		
							C	C	C
							A	A	T
							C	GACTCATCA	GC
									TCT
							A	TTGAGTAGT	CG
GAM23	<u>470</u>	FE65L2	5'	AGGCCTGATGAGTTCA	238		GGA		
							C	C	C
							A	A	T
							C	GACTCATCA	GC
									TCT
							A	TTGAGTAGT	CG
GAM23	<u>469</u>	FGFR4	3'	AGAGAACCTGAAAGCCTG	193		C	C	C
							A	CA	A
							CAG	CT	TC
									AGCTTCTCT
							GTC	GA	AG
GAM23	<u>469</u>	FGFR4	3'	AGAGAACCTGAAAGCCTG	58		TCGAAGAGA		
							C	—	G
							A	CA	A
							CAG	CT	TC
									AGCTTCTCT
							GTC	GA	AG
GAM23	<u>472</u>	FHL1	3'	AGAGAACCTGATGCCCTC	55		TCGAAGAGA		
							C	—	G
							CT	—	A
							GA	CATCA	GCTTCTCT
							CT	GTAGT	CGAAGAGA
GAM23	<u>469</u>	GCNT2	5'	AGAGAACCGAGTGAGTTG	56		CC		
							CAAGC		
							CAGACTCAT		TTCTCT
							GTTTGAGTG		AAGAGA
GAM23	<u>469</u>	GNRHR	5'	AGAGAACCTGGTAATTCTG	38		AGCA		
							CTC	A	
							CAGA	ATCA	GCTTCTCT
							GTCT	TGGT	CGAAGAGA
GAM23	<u>470</u>	HIS1	5'	AGGGGAGATGAGTTG	105		TAA		
							AAG		
							CAGACTCATC		CTTCT
							GTTTGAGTAG		GGGGA
GAM23	<u>469</u>	HNRPD	3'	AGAAAGGTATGAGTTG	92		A		
							CAA	C	
							CAGACTCAT		GCTT
									TCT

GAM23	<u>469</u>	INHBA	3'	AGAAAGCCATGAGTTTG	59	GTGGAGTA TGGA AGA CAA A CAA C CAGACTCAT GCTT TCT GTGGAGTA CGAA AGA C - G C CA CA ACT AT AGCTTCTCT GT TGA TA TCGAAGAGA G A C - ACT T A CAG CA CA GCTTCTCT GTC GT GT CGAAGAGA CC - C AC CAA CAG TCAT GCTTCTCT GTC AGTG TGAAGAGA CC ACTC A CAG ATC AGCTTCTCT GTC TAG TTGAAGAGA C A TCATC CAGAC AAGCTTCTCT GTTTG TTCGAAGAGA TAC - TCATC CAGAC AAGCTTCTCT GTTTG TTCGAAGAGA TAC - AA CAGACTCATC GCT TCT GTCTGAGTAG TGA AGA A C AAG C CAGACTCATC CCT TCT GTCTGAGTAG GAA AGA GG - A AA CAG CTCATC GCTTCTCT GTC GAGTAG CGAGGGGA - - CTC ATCAAGCTTCTCT GAG TAGTTCGAAGAGA GTTC T A CAGAC CATCA GCTTCT GTCTG GTAGT CGGAGA T AGC GACTCATCA TTCTCT TTGAGTAGT AAGAGA GT - C AT GA TC CAAG CTTCTCT CT AG GTTC GAAGAGA
GAM23	<u>469</u>	KIF3B	3'	AGAGAAGCTCATAAGTGTG	87	
GAM23	<u>469</u>	MSN	3'	AGAGAAGCCTGTGCCCTG	262	
GAM23	<u>469</u>	MTR	3'	AGAGAAGTGTGACCCTG	36	
GAM23	<u>469</u>	PCDHB9	3'	AGAGAAGTTAGATCCTG	169	
GAM23	<u>469</u>	SMARCA3	3'	AGAGAAGCTTCATGTTTG	246	
GAM23	<u>469</u>	SMARCA3	3'	AGAGAAGCTTCATGTTTG	66	
GAM23	<u>470</u>	SMG1	3'	AGACAGTAGATGAGTCTG	138	
GAM23	<u>469</u>	SNCAIP	5'	AGAAAGGGGGTGAGTCTG	399	
GAM23	<u>469</u>	SYNGR1	3'	AGGGGAGCGATGAGCTG	86	
GAM23	<u>474</u>	UCP2	5'	AGAGAAGCTTGATCTTGGAG	68	
GAM23	<u>470</u>	BMF	3'	AGAGGCTGATGTGTCCTG	229	
GAM23	<u>472</u>	BNIP2	3'	AGAGAATGTGATGAGTT	278	
GAM23	<u>472</u>	DDX33	3'	AGAGAAGCCTTGGAAC	171	

GAM23	<u>475</u>	EML4	3'	AGAAACTTGGATGAGTT	168	A — C GACTCATC — AAG TTCT TTGAGTAG TTC AAGA GT A CAAG
GAM23	<u>471</u>	EPB41L4	3'	AGAGAAGAAATGGGTCT	187	AGACTCAT CTTCTCT TCTGGGTA GAAGAGA
GAM23	<u>469</u>	FLJ11588	5'	AGAGAACAGAACGGCCTG	199	AA A CA AA CAG CT TC GCTTCTCT GTC GG AG CGAAGAGA
GAM23	<u>471</u>	FLJ20150	3'	AGAGAACCTGTGGCT	153	C CA A A T T A AG C CA CA GCTTCTCT TC G GT GT CGAAGAGA
GAM23	<u>470</u>	FLJ20507	3'	AGATGTTGATGAGGCTG	154	— C — A G T CAG CTCATCAA C TCT GTC GAGTAGTT G AGA
GAM23	<u>470</u>	FLJ20507	3'	AGATGTTGATGAGGCTG	261	G T A G T CAG CTCATCAA C TCT GTC GAGTAGTT G AGA
GAM23	<u>469</u>	FLJ20972	3'	AGAGAACAGTTGGCATCTG	205	G T C_ TCAA CAGA TCA GCTTCTCT GTCT GGT CGAAGAGA
GAM23	<u>472</u>	FLJ22233	3'	AGAGAACGCTAGAACGTC	204	AC TGA CA A GACT TC AGCTTCTCT CTGA AG TCGAAGAGA
GAM23	<u>469</u>	FLJ23191	3'	AGAGAACGTTGTGACCTG	198	A AC CA CAG TCAT AGCTTCTCT GTC AGTG TTGAAGAGA
GAM23	<u>469</u>	FLJ23468	5'	AGAGAACACCAGCTGAGTCTG	200	C — TCAA CAGACTCA GCT TCTCT GTCTGAGT CGA AGAGA CCAA
GAM23	<u>471</u>	GIT2	3'	AGAGAACCATCAGTCT	133	C CAA AGACT AT GCTTCTCT TCTGA TA CGAAGAGA
GAM23	<u>471</u>	GIT2	3'	AGAGAACCATCAGTCT	231	C C CAA AGACT AT GCTTCTCT TCTGA TA CGAAGAGA
GAM23	<u>471</u>	GIT2	3'	AGAGAACCATCAGTCT	232	C C CAA AGACT AT GCTTCTCT TCTGA TA CGAAGAGA
GAM23	<u>471</u>	GRID1	3'	AGAGAACCTAGGTGGGCT	285	C A AA AG CTCATC GCTTCTCT TC GGGTGG CGAAGAGA ATC

GAM23	<u>473</u>	GT650	3'	AAGCTTTCTATGAGTTG	230	C CAGACTCAT GTTTGAGTA	AAGCTT TTCGAA
GAM23	<u>470</u>	IKKE	3'	AGGACTGTGAGTC	124	TCT CA C CAGACTCAT GTCTGAGTG	AG TTCT TC AGGA
GAM23	<u>472</u>	KIAA0254	5'	AGAGGACCGCGATGAGTC	131	AA GACTCATC CTGAGTAG	— GC TTCTCT CG AGGAGA
GAM23	<u>469</u>	KIAA1026	3'	AGAGAACGCTGCCTCAGTC	292	CATCA CAGACT GTCTGA	— AGCTTCTCT TCGAAGAGA
GAM23	<u>472</u>	KIAA1163	3'	AGAGAACATGTCTGAGTT	331	CTCCG T A GACTCA TTGAGT	CA GCTTCTCT GT CGAAGAGA
GAM23	<u>470</u>	KIAA1598	3'	AGAACGCTCTGGGTCTG	161	CT A TC CAGACTCA GTCTGGGT	— AAGCTTCT TTCGAAGA
GAM23	<u>470</u>	KIAA1853	3'	AGAACGATGGGTCTG	287	TTTGTC CAA CAGACTCAT GTCTGGTA	— GCTTCT CGAAAGA
GAM23	<u>472</u>	LOXL4	3'	AGAGAACGCTGGGATC	213	A CT A GA CATCA CT GTGGT	— GCTTCTCT CGAAAGAGA
GAM23	<u>469</u>	METAP1	3'	AGAGAACGCTGAAGTTG	298	AG CA A CAGACT TCA GTTTGA AGT	— GCTTCTCT CGAAAGAGA
GAM23	<u>472</u>	MGC11034	3'	AGAGAACGCTCTTGAAGTT	211	G — TCA GACT CA AGCTTCTCT TTGA GT TCGAAGAGA	— GCTTCTCT CGAAAGAGA
GAM23	<u>470</u>	MGC14128	3'	AGAACGCTTGAGAGCCTG	222	A TTC A A — CAG CTC TCAA GCTTCT GTC GAG AGTT CGAAGA	— GCTTCTCT CGAAAGAGA
GAM23	<u>470</u>	MGC16175	5'	AGAGGCTGTGAGTC	219	C — T CA CAGACTCAT AGCTTCT GTCTGAGTG TCGGAGA	— CA GCTTCTCT CGAAAGAGA
GAM23	<u>472</u>	MGC2752	5'	AGAGAACGCTCAGTAGAAC	327	C — CA GA TC AT AGCTTCTCT CT AG TG TCGAAGAGA	— GCTTCTCT CGAAAGAGA
GAM23	<u>469</u>	MGC34923	3'	AGAGAACGCTGAAGAGCCTG	254	A A AC A A AA CAG CTC TC GCTTCTCT GTC GAG AG TGAAGAGA	— GCTTCTCT CGAAAGAGA
GAM23	<u>469</u>	NR1I3	5'	AGAGAACGAGGTCTG	89	C A GA ATCAA	— ATCAA

						CAGACTC GTCTGAG	GCTTCTCT CGAAGAGA
GAM23	<u>469</u>	NYD-SP15	3'	AGAGAAGAAATATTGAGTCTG	208	GA TCAAG	
GAM23	<u>469</u>	OSBPL8	5'	AGAGAAGTTGGGTCTG	177	CAGACTCA GTCTGAGT	CTTCTCT GAAGAGA
GAM23	<u>469</u>	PLEKHA4	5'	AGAGACCCCTGTGAGTCTG	178	TTATAAA ATCAA	
GAM23	<u>469</u>	PRKWNK2	3'	AGAGATGATTGAGTCTG	372	CAGACTC GTCTGGG	GCTTCTCT TGAAGAGA
GAM23	<u>469</u>	PSMD4	3'	AGGGTAGCTGAGTCTG	63	GT CA CT	
GAM23	<u>469</u>	RIS1	3'	AGAGAAGCTTTGTATCTG	337	CAGACTCAT GTCTGAGT	AG TCTCT TC AGAGA
GAM23	<u>469</u>	RNF24	3'	AGAGGAGTGGATGAGCCTG	114	T TCAA T	
GAM23	<u>469</u>	SNURF	3'	AGAAAAGCGGGTTTGGGTCTG	96	CAGACTCA GTCTGGGT	GCTTCTCT TCGAAGAGA
GAM23	<u>469</u>	SULT4A1	3'	AGAGAAGCTGTGTTTTG	284	AT TTC A AA	
GAM23	<u>469</u>	SV2B	3'	AGAGAATTGTGTGAGTCTG	135	CAG CTCATC GTC GAGTAG	GCTTCTCT TGAGGAGA
GAM23	<u>469</u>	SZF1	5'	AGAGAAGCCTAGATATCTG	147	C TCAA C	
GAM23	<u>469</u>	TLR10	5'	AGAGAGGGTATTGAGTCTG	210	CAGACTCAT GTCTGAGT	GCTTCTCT CGAA AGA
GAM23	<u>472</u>	ZNF185	3'	AGAGGAGCTGTGAATC	111	TTTGGG A	
GAM23	<u>470</u>	LOC113612	3'	AGAAGGATGAGTTG	300	CT T C AA	
						CAGACTCATC GTCTGAGT	TTCTCT AAGAGA
						CAGACTCA GTCTGAGT	CTTCTCT GGAGAGA
						TATG C T	
						GA TCA CAAGCTTCTCT CT AGT GTTCGAGGAGA	
						A — CAGACTCATC	AAG CTTCTCT

				 GTTTGAGTAG	 GAAGA
GAM23	<u>472</u>	LOC133539 3'	AGAGAAGCCCAGGATGGTC	312	T AA GAC CATC GCTTCTCT CTG GTAG CGAAGAGA
GAM23	<u>469</u>	LOC139221 5'	AGAGAAGCACATGACCTG	313	GACC AC CAA CAG TCAT GCTTCTCT GTC AGTA CGAAGAGA C CA
GAM23	<u>473</u>	LOC142941 3'	AAGTTTATTGTAATGAGTCTG	345	CAGACTCAT CAA GCTT GTCTGAGTA GTT TGAA AT ATT AA T
GAM23	<u>469</u>	LOC145717 5'	AGAGAGTGGGGTGAGTCTG	279	CAGACTCATC GCT CTCT GTCTGAGTGG TGA GAGA
GAM23	<u>469</u>	LOC147229 3'	AGAGAAGCTGGCAAGAGCTG	325	GGG A ATCA CAG CTC AGCTTCTCT GTC GAG TCGAAGAGA
GAM23	<u>472</u>	LOC147658 3'	AGAAAAGTTGAAGTC	326	AACGG - CA C GACT TCAAGCTT TCT CTGA AGTTTGAA AGA A
GAM23	<u>471</u>	LOC147920 3'	AGAGAAGCCTGAGGAATTT	328	C A A AGA TC TCA GCTTCTCT TTT AG AGT CGAAGAGA
GAM23	<u>469</u>	LOC148894 5'	AGAGAAGCTCCGTGGGCCTG	347	A G C A CA CAG CTCAT AGCTTCTCT GTC GGGTG TCGAAGAGA
GAM23	<u>469</u>	LOC150606 3'	AGAGAAGCTGGGTGATCTG	349	C CC C A CAGA TCATC AGCTTCTCT GTCT AGTGG TCGAAGAGA G
GAM23	<u>472</u>	LOC150606 3'	AGAGAAGCTTGTC	350	T T GAC CA CAAGCTTCTCT CTG GT GTTCGAAGAGA
GAM23	<u>471</u>	LOC152220 3'	AGAGTATTTCTTGATGAATTT	351	C CTT AGA TCATCAAG CTCT TTT AGTAGTTC GAGA
GAM23	<u>469</u>	LOC155382 3'	AGAGAAGCTGCAGGAGCTG	356	A TTTAT A ATCA CAG CTC AGCTTCTCT GTC GAG TCGAAGAGA
GAM23	<u>471</u>	LOC157621 3'	AGAGGGCGAAATGAGTCT	358	GACG - CAA T AGACTCAT GCT CTCT TCTGAGTA CGG GAGA
GAM23	<u>469</u>	LOC161528 5'	AGAGAGTGGGGTGAGTCTG	342	AAG AA T CAGACTCATC GCT CTCT

GAM23	<u>469</u>	LOC197114 5'	AGAGAAGCCCGAGGGGGCTG	369	GTCTGAGTGG GGG A A AA CAG CTC TC GCTTCTCT GTC GGG AG CGAAGAGA G G CC	-
GAM23	<u>472</u>	LOC199883 3'	AGAAAGGCGGTGAGTC	370	GACTCATC CTGAGTGG AA GCTT TCT CGGA AGA	C
GAM23	<u>472</u>	LOC200020 3'	AGAAAGGCGGTGAGTC	371	GACTCATC CTGAGTGG AA GCTT TCT CGGA AGA	A
GAM23	<u>472</u>	LOC200226 3'	AGAGAAGCTCGTGAATGTT	365	GAC — TCAT TTG AGTG CA AGCTTCTCT TCGAAGAGA	CA
GAM23	<u>469</u>	LOC204820 5'	AGAGAAGCCAGGCCAGCTG	373	TA C A CA AA CAG CT TC GCTTCTCT GTC GA GG CGAAGAGA	—
GAM23	<u>472</u>	LOC219392 5'	AGAGAAATCCTAGATGAGTC	377	— CC AC — A C — GACTCATC AG TTCTCT CTGAGTAG TC AAGAGA	—
GAM23	<u>471</u>	LOC219800 3'	AGAGAAGCTTGGGAGCCT	389	A A AG CTC TCAAGCTTCTCT TC GAG GGTCGAAGAGA	A
GAM23	<u>469</u>	LOC220753 5'	AGAGAAGCCAGAGGTGTG	388	C G CA AA CA ACT TC GCTTCTCT GT TGG AG CGAAGAGA	—
GAM23	<u>469</u>	LOC220776 3'	AGAGGGGTGATGATAAACTG	283	G AC — AC CAG TCATC GCTTCTCT GTC AGTAG TGGGGAGA	AAAT
GAM23	<u>469</u>	LOC221454 5'	AGAGAAGATGAAAGTTG	382	CA AG CAGACT TCA CTTCTCT GTTGA AGT GAAGAGA	—
GAM23	<u>472</u>	LOC222444 3'	AGAGAAGCCCAGGATGGTC	392	A A T AA — GAC CATC GCTTCTCT CTG GTAG CGAAGAGA	—
GAM23	<u>469</u>	LOC222962 3'	AGAGGGAGGTAAAGTCTG	387	GACC — C AAG CAGACT ATC CTTCTCT GTCTGA TGG GGGGAGA	—
GAM23	<u>469</u>	LOC245727 5'	AGAGAGTGGGGGTGAGTCTG	376	A A AA — T CAGACTCATC GCT CTCT GTCTGAGTGG TGA GAGA	—
GAM23	<u>469</u>	LOC253525 5'	AGAGAAGCTGCAGGTTG	401	GGG CATCA CAGACT AGCTTCTCT GTTTGG TCGAAGAGA	—

GAM23	<u>469</u>	LOC254249 5'	AGAGAAGTTGTAAATTG	397	ACG CTCAT CAGA CAAGCTTCTCT GTTT GTTTGAAGAGA
GAM23	<u>469</u>	LOC255475 5'	AGAGAAGCCGAGCTCTG	403	AAAT ATCAA CAGA CTC GCTTCTCT GTCT GAG CGAAGAGA
GAM23	<u>476</u>	LOC51026 3'	AGAACCTTGATGAGACT	146	A C C A AG CTCATCAAG TTCT TC GAGTAGTTC AAGA
GAM23	<u>470</u>	LOC91308 5'	AGAAGAGATGAGTTG	274	A CC AAG CAGACTCATC CTTCT GTTTGAGTAG GAAGA
GAM24	<u>523</u>	CASP10 3'	ATACAACCTGATGTCATATTCC 223, <u>524</u>	C C A III	TG GA AC CAG TTGTA T AC CT TG GTC AACAT A
GAM24	<u>523</u>	CASP10 3'	ATACAACCTGATGTCATATTCC 224, <u>524</u>	C C A III	TATAC TA C III TG GA AC CAG TTGTA T AC CT TG GTC AACAT A
GAM24	<u>477</u>	CHRN B3 5'	TTGGGTTCCACTTCGGA	49	TATAC TA C III A A C TCC AA TG GAACCCAG AGG TT AC CTTGGGTT C C - G C TGC AA CCAGATTGTA ATG TT GGTCTAACAT
GAM24	<u>478</u>	LANCL1 3'	TACAATCTGGACTTGGTA	100	G CA A GC T CA AAT GAACCCAGAT GT GT TTA CTTGGGTCTA CA C AA CCA ATGCGAAC GATTGTA TACGCTTG TTAACAT
GAM24	<u>479</u>	MS4A3 3'	ACATCTGGTTCAAATTCTG	101	ACCCTG A C AGA TCCA AATGCGAA CC TTGTA GGGT TTACGCTT GG AACAT C TA -
GAM24	<u>480</u>	SLC1A4 3'	TACAATTGTCCCAGTCGCAT	64	A TCCAAATG GAACCCAG AGGTTTAC CTTGGGTC A A C A TCCA AATG GA CCCAG AGGT TTAC CT GGGTT C C TCCAAATG GA CCCAG AGGTTTAC CT GGGTT C GA
GAM24	<u>25</u>	ALLC 5'	TACAAGGATTTCGCATTCTGGG	162	
GAM24	<u>477</u>	APOL6 3'	CTGGGCTCACATTGGAA	206	
GAM24	<u>477</u>	CBX6 3'	TTGGGCTCCATTCTGGA	128	
GAM24	<u>477</u>	FLJ10055 3'	TTGGGAGTCCCATTGGAA	156	

GAM24	<u>481</u>	FLJ22059	5'	CAGTCTGGACCAGCACCTTGGA	191	AA TCCAA AGGTT CC A	GAAC TGC ACG ACCA C C	CCAGATTG GGTCTGAC A TCCA AGGT C
GAM24	<u>477</u>	KCNH8	3'	TTGGGTTCACATTCTGGA	252	TCCA AGGT C	AATG TTAC A	GAACCCAG CTTGGGTT A
GAM24	<u>477</u>	KIAA0870	3'	TTGGGTCTGCATTTGGA	339	TCCAAAATGCG AGGTTTTACGT	ACCCAG TGGGTT C	A A C CCCAG
GAM24	<u>482</u>	KIAA1157	3'	ACAGTATTCCATTTGGA	296	TCCAAAATG AGGTTTTAC	GAA CTT	ATTGT TGACAA
GAM24	<u>483</u>	PRO1048	3'	ACAATGAGTTGCAATT	163	— AAAATGCGAAC TTTTACGTTTG	A C GA	A CA TTGT AACA
GAM24	<u>479</u>	PRO1787	3'	ACAATTCCGCATTTG	165	AAAATGCG GTTTTACGC	— AACCCA GATTGT TTAACAA	A A —
GAM24	<u>484</u>	UBE2G1	3'	TACAGATGATTACGCATTTG	67	C CAAATGCG GTTTTACGC	— AACC CA	GA TTGTA GACAT
GAM24	<u>25</u>	LOC122402	3'	TACTTCTGGTTCACATTTGG	306	A ATTA C	A GAACC C	A AGA TT CAT
GAM24	<u>485</u>	LOC153592	3'	GGAATTTCAGCATTGGA	355	A TCCAAAATGC — AGGTTTTACG	T GAA C CTT	T CC GG
GAM24	<u>482</u>	LOC256158	5'	ACAATCTGAACGTCTGGG	404	A AAAT TCCA GGGT	A AACC GCG TGC	AA GTA TT CAT
GAM25	<u>486</u>	ITGA5	3'	CTCAGATCCAGGGACAGAGG	264	C GTTAGA TCTCTG GGAGAC	AA A CC AG AG AG	AA CC GATCTGAG CTAGACTC AC CCAGA —
GAM25	<u>487</u>	SF3B3	3'	GCTCTAGAACATCTAACAGA	116	TCTGGTTAGA AGACCAATCT	TCT GAGC AGA CTCG	GAGC — TCTGAGC — AGA CTCG
GAM25	<u>487</u>	SLC4A4	3'	GCTCAGAGTTGTTAACAGA	71	A AC TCTGGTTAG AGACCAATT	A A CAG TCTGAGC GTT AGACTCG	T T GAGC AC T
GAM25	<u>486</u>	ZNF180	3'	CTCAGACCTGAATCAGAGA	120	G AGAC TCTCTGGTT AGAGACTAA	A A CAG TCTGAG GTC AGACTC	G AGAC A C
GAM25	<u>487</u>	AP1G2	5'	GCCCAGGCCAGCCCCGACCAGAG	233	C AGACCAGA —	AGACCAGA —	A

				A			
GAM25	<u>488</u>	BCL2L1	3'	GCCCAGATCTGGTCCCTTCAG	241	TCTCTGGTT AGAGACCAG GTTA_	TCTG GC GGAC CG CCCGCAC_ C A
GAM25	<u>486</u>	FLJ25012	5'	CTCAGATCTGAAAAGCACAAGA	250	CTG GAC	GACCAGATCTG GC CTGGTCTAGAC CG GTTCC C _ AGAC TCT TG GTT CAGATCTGAG AGA AC CGA GTCTAGACTC A AAA_ C GG
GAM25	<u>489</u>	FLJ31952	3'	CAAATCTGGTTCTGAAAG	253	CT GA	TTAGA CCAGAT TG AGTCT GGTCTA AC A_ T A G_ A
GAM25	<u>490</u>	MDS025	3'	CTCAGACCTGGTTTGAGATAGA	184	TCTG AGAT	TTAGACCAG TCTGAG AGTTGGTC AGACTC AG C GGTT AC_
GAM25	<u>487</u>	MGC32043	3'	GCTCAGATCTGATGCTTCAGA	249	TCT AGA	AG CAGATCTGAGC TC GTCTAGACTCG ACT_ GTA AGACCA CT_
GAM25	<u>486</u>	MSI2	3'	CTCCCCATCCAACCAGAGA	245	TCTCTGGT AGAGACCAA	GAT GAG CTA CTC CC CCC
GAM25	<u>487</u>	ZNF271	5'	GCTCAGATCTGGTAAACATCA	395	TCTCTG AGAGAC	A GTT GACCAGATCTGAGC CAA TTGGTCTAGACTCG TA A
GAM25	<u>487</u>	LOC144508	5'	GCTCAGATCCATGTGCCAGGG	362	TCTCTGGT AGGGACCG	TAGACCA GATCTGAGC CTAGACTCG TGTAC_
GAM25	<u>486</u>	LOC145845	3'	CTCAAATCCCACCAAGAGA	346	TCTCTGGT AGAGACCA	C GAT TGAG CTA ACTC CC A
GAM26	<u>491</u>	CDH19	3'	GAAAATTAAAGGAGCAA	182	TTGC AACG	A CTTTAAATTTTC GAAATTAAAAG AG
GAM26	<u>492</u>	CRYGS	5'	TGGGAAAACCAGTCTATGCACC	152	TTGGT GCA AACCA CGT	T CTTAAA_ TTTTCCA ATCTGACC - C A_
GAM26	<u>493</u>	CYP1B1	3'	GAAAATTGAAAAGTACAACCAA	33	TTGGTTG AACCAACGT	TTTTTC AATCAAC TGAAA TTAAAAG A AG C AAA
GAM26	<u>494</u>	GLI3	3'	GGAAAAAAAGACTGCAACCAA	35	TTGGTTGCA AACCAACGT	TTTTCC AGA AAAAGG C AA_
GAM26	<u>493</u>	PCLO	3'	GAAGATAATGCAACCAA	391	TTGGTTGCA	CTTTAA_ ATTTTC

							AACCAACGT	TAGAAG
GAM26	<u>492</u>	PPP2R5A	3'	TGGGAAAGTAAACCAA	102		AA	
							GC	TAAATTT
							TTGGTT	ACTT
								TCCCA
							AACCAA	TGAA
								AGGGT
GAM26	<u>492</u>	PTER	3'	TGAGAAAATTAAAGTGTCT	207		A	
				AG			TT	C
							TTGG	GCACTTAAATTTTC
								CA
							GATC	TGTGAAATTAAAG
							TT	GT
GAM26	<u>495</u>	RFX5	3'	GGGAAAAGCAGTAAACCAA	39		GC	TTAAA
							TTGGTT	ACT
								TTTTCCC
							AACCAA	TGA
								AAAAGGG
GAM26	<u>494</u>	CSMD1	3'	GGAGTATTAAAGTGGAACCAA	301		A	CG
							G	ATT
							TTGGTT	CACTTAA
								TTCC
							AACCAA	GTGAAATT
								GAGG
GAM26	<u>493</u>	MGC15438	3'	GAAAGAAAGCGCAGCCAA	220		G	AT
							A	AAA
							TTGGTTGC	CTTT
								TTTTC
							AACCGACG	GAAA
								GAAAG
GAM26	<u>494</u>	NYD-SP18	3'	GGAGAAAATGCAACCAA	217		C	C
							TTGGTTGCA	TTT
								TTTTCC
							AACCAACGT	AAA
								AGAGG
GAM26	<u>494</u>	OLFM3	3'	GGAAAAATAATGTAACCAA	340		C	TAAA
							TTGGTTGCA	TT
								TTTTCC
							AACCAATGT	AA
								AAAAGG
GAM26	<u>495</u>	RPL13A	3'	GGGAAGATGCACAACCAA	115		TA	
							TTGGTTG	CACTTTAA
								ATTTTCCC
							AACCAAC	
								TAGAAGGG
GAM26	<u>496</u>	LOC129452	3'	AGAATGGACAAGCGCAACCAA	310		ACG	
							A	TAA
							TTGGTTGC	CTT
								ATTTT
							AACCAACG	GAA
								TAAGA
							C	CAGG
GAM26	<u>494</u>	LOC150197	3'	GGATTAAAGTGGAACCAA	335		G	ATTT
							TTGGTT	CACTTTAA
								TCC
							AACCAA	GTGAAATT
								AGG
							G	
GAM26	<u>494</u>	LOC162239	3'	GGAAATTATAATGGCAACCAA	344		AC	AAT
							TTGGTTGC	TTTA
								TTTCC
							AACCAACG	AAAT
								AAAGG
							GT	ATT
							TTGGTTGCA	TAA
								ATTTT
							AACCAACGTGAA	TAAAG
							CGG	
GAM26	<u>496</u>	LOC219972	3'	GAAATGGCAAGTGCACCAA	379		C	CCC
							GG	C
							AACGA	CT
								GTCACAAT
							CC	TTGTT
								GA
								CAGTGTAA
							A	AA
								A
GAM27	<u>497</u>	DDX6	3'	ATTGTGACAAGAATTGTTACC	80		AA	
							TTGGCAAC	GACCC
								CT
								GT
GAM27	<u>498</u>	LOC126917	3'	GCAGTGGGTCTGTTGCCA	309		C	

GAM27	<u>499</u>	LOC170395	3'	TATTGTTCTGGGTGTTGCCA	316	ACCGTTG CTGGG GA CG T T G CTCGTC TGGCAAC ACCC ACAATA ACCGTTG TGGG TGTTAT TCTT—
GAM28	<u>500</u>	ABCC3	3'	TGCCCTGGCTGTGCTCTAC	170	GTG AG ACA CCAGGGCA CAT TC TGT GGTCGGT C G C AGAAC— GTGC ATCCAGGGCA TACG TAGGTCCCCGT
GAM28	<u>500</u>	CASP3	3'	TGCCCTGGATCTACCAGCAT	225	ACCATC AGAAC— GTGC ATCCAGGGCA TACG TAGGTCCCCGT
GAM28	<u>500</u>	CASP3	3'	TGCCCTGGATCTACCAGCAT	79	ACCATC CA AC TAGTG GA ATCCAGGG ATCAC CT TAGGTCCC
GAM28	<u>501</u>	EMS1	3'	CCCTGGATCCTCACACTA	90	A— CC CA AC TAGTG GA ATCCAGGG ATCAC CT TAGGTCCC
GAM28	<u>501</u>	EMS1	3'	CCCTGGATCCTCACACTA	240	A— CC CA— GTG GAACA TCCAGGGCA CAT TTTGT AGGTCCCCGT
GAM28	<u>500</u>	MLLT2	3'	TGCCCTGGACATGTTCCCTAC	97	CC AC G CA TAGT CAG AACATC GGGGCA GTCG GTC TTGTAG CCCCGT
GAM28	<u>502</u>	TACC1	3'	TGCCCTTGGAGATGTTCTGGCT	104	G C AC T C CA A AGTG AGAACATC GG A TCAC TCTTGTGG CC
GAM28	<u>503</u>	TNFSF6	3'	CCAGGTGTTCTACACTCA	42	C A A— AC— TATAGTGCAGA AT CCA ATATCACGTCT TA GGT
GAM28	<u>504</u>	UBB	3'	TGGCATTACTCTGCACTATA	166	CAT C CA— AGTGCAGAA TCCA GGGGCA TCACGTCTT AGGT CCCCGT
GAM28	<u>505</u>	AKAP10	3'	TGCCCTTTGGAATTCTGCACT	113	A— TT TCC GTGCAGA ACA AGGGGC CACGTCT TGT TCCCG
GAM28	<u>506</u>	DECR2	3'	GCCCCCTCTGTCTCTGCAC	176	C C CA A TC TAGTG GA CA CAGGGGC ATCAC CT GT GTCCCCG
GAM28	<u>507</u>	KIAA0240	3'	GCCCCCTGTGTCCCACTA	383	C — — A— GTG CAGAA C TCCAGGGC CGC GTCTT G AGGTCCCCG
GAM28	<u>506</u>	MGC16385	5'	GCCCCCTGGACGTTCTGCCGC	255	

GAM28	<u>508</u>	MGC5139	5'	GCCCCCTGGGCACACTGTA	305	C T C CAGAACAA TATAGTG ATGTCAC TCCAGGGC GGGTCCCCG
GAM28	<u>509</u>	P5-1	3'	CCCCTGGATGCCCTAACCACT	110	AC C AA AGTG AG CATCCAGGG GTAGGTCCCC TCAC TC CAA CCC T AACA TAG GCAG TCCAGGG GGGTCCCC
GAM28	<u>510</u>	TED	3'	CCCCTGGCCCTGCCTA	143	T ATC CGTC — CC — ACATCCA TAGTGAGA ATCAGTCT GGGGCA TCTCGT
GAM28	<u>502</u>	LOC133418	3'	TGCTCTAAAGCTCTGCACTA	311	CGAAA CATCC AGTGCAGAA TCACGTCTT AGGGGC TTCCCG
GAM28	<u>512</u>	LOC158677	3'	TGCCCCTGGATATCAGCAATAT	360	A TATA TGC GA ATCCAGGGCA ATAT ACG CT TAGGTCCCCGT A A A AA TC — — — — —
GAM28	<u>501</u>	LOC221715	3'	CCACTGTGCTTGCACTA	390	TAGTGCA ATCACGTT GAGGCA TCTCGT CA A A TAGTGAGA ATCACGTCT AT CACGTCT TA GGT — — — — —
GAM28	<u>504</u>	LOC254746	3'	TGGCATTACTCTGCACTATA	394	CAT C ACATCCA TATAGTGAGA ATCACGTCT AT CACGTCT TA GGT — — — — —
GAM28	<u>502</u>	LOC255098	3'	TGCTCTAAAGCTCTGCACTA	396	CGAAA ACATCCA TAGTGAGA ATCACGTCT GGGGCA TCTCGT
GAM29	<u>513</u>	ADAM19	3'	CTGATGGAGATGCTCAAGGC	228	AG TATGG GCCTT GCATCTCC CAG CGGAA CGTAGAGG GTC CT TA — — — — —
GAM29	<u>514</u>	LFG	3'	TGCCACAGGCCTAACCGCT	319	ATCTC A AGCCTTAGGC CT TGGCA GA ACCGT TCGGAATCCG C — — — — —
GAM29	<u>515</u>	NOLA2	5'	GGAAGTGATGCCTAAAGCT	393	C AGC TTAGGCATC TCC TCG AATCCGTAG AGG A TGA — — — — —
GAM29	<u>514</u>	FLJ10751	3'	CCAGAGACACCTGAGGC	158	CA CTA GCCTTAGG TCTC TGG CGGAGTCC AGAG ACC A AC — — — — —
GAM29	<u>514</u>	FLJ10751	3'	CCAGAGACACCTGAGGC	159	CA CTA GCCTTAGG TCTC TGG CGGAGTCC AGAG ACC AC — — — — —

GAM29	<u>513</u>	FLJ10925	5'	CTGCCCCCAGGGACACCTAAGG	160	CA T AT GCCCTTAGG TC CCT GGCAG CGGAATCC AG GGA CCGTC
GAM29	<u>517</u>	KIAA1118	3'	GTGGTTGAGATGCCACGGCT	289	AC - CCC TTA CT G AGCC GGCATCTC AT GC TCGG CCGTAGAG TG TG
GAM29	<u>518</u>	KIAA1649	3'	CTGCCATTCTGTGCCTAGGCT	215	CAC T G T CTCCT AGCCT AGGCAT ATGGCAG TCGGA TCCGT TACCGTC
GAM29	<u>513</u>	LIMR	3'	CTGCCATCTGTGCCTAGGC	157	TCTT T TCTCCT GCCT AGGCA ATGGCAG CGGA TCCGT TACCGTC
GAM29	<u>516</u>	MGC14161	5'	CCAGAGAGATGCCAAAGC	221	CGTC - A CTA GCCCT GGCATCTC TGG CGGAA CCGTAGAG ACC
GAM29	<u>519</u>	NJMU-R1	3'	CATGAAGAAATGCCTGAAGC	188	A AG C C C GC TTAGGCAT TC TATG CG AGTCCGTA AG GTAC
GAM29	<u>518</u>	SEMA3E	3'	CTGTTGTGAGAAATGCCAGGC	119	A AA TA C C TG AGCCT GGCAT TC TA GCAG TCGGA CCGTA AG GT TGTC
GAM29	<u>520</u>	YKT6	3'	CTGCCATAGATAACCCTAAG	106	C A A GT CATCTC CTTAGG CTATGGCAG GAATCC GATACCGTC
GAM29	<u>521</u>	LOC142972	5'	GCCACAGGAGATGCCAAAGC	271	CATA C A A GC TT GGCATCTCCT TGGC CG AA CCGTAGAGGA ACCG
GAM29	<u>514</u>	LOC143689	3'	TGCCATAAGCTCAAGGCT	318	A C C AG ATCTCC AGCCTT GC TATGGCA TCGGAA CG ATACCGT
GAM29	<u>522</u>	LOC148930	5'	CCATAGGGAGCCTAAG	332	CT A A T CTTAGGC TC CCTATGG GAATCCG AG GGATACC
GAM29	<u>516</u>	LOC220469	3'	CCAAGGGATGCCAAAGC	317	C A T A GC TT GGCATC CCT TGG CG AA CCGTAG GGA ACC
GAM29	<u>519</u>	LOC253782	3'	CATAAGAGCACCTAAGGC	398	A C CAT C GCCTTAGG CTC TATG CGGAATCC GAG ATAC
GAM29	<u>514</u>	LOC92078	5'	TGCCCAGAGGCCTAAGGCT	282	AC A A CCTAT AGCCTTAGGC TCT GGCA TCGGAATCCG AGA CCGT